

• Appln. No. 09/856,298
Amdt. dated August 20, 2003
Reply to Office action of June 23, 2003

REMARKS

Claims 55-57 and 59-85 are presently pending. The examiner considers that this application contains 44 groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1 and requires restriction to a single invention or group. The examiner states that inventions of Group 1-14 lack unity of invention, each with the other, because the claims common to each group describe as many as fourteen separate and distinct peptide or polypeptide, each is disclosed to have a special technical feature defined by its primary structure of a native peptide, protein, or domain, which need not comprise the amino acid sequence of any other disclosed, mature, polypeptide or peptide that might be considered to link any one of them to another.

Applicants provisionally elect Group 1 (SEQ ID NO:2), presently comprising claims 76, 77, 55-57, 59, 82 and 83, with traverse. The restriction requirement is traversed insofar as Groups 1-3 and 10 are concerned. Applicants request that Groups 2, 3 and 10 be rejoined with Group 1 for prosecution on the merits because the structure of SEQ ID NOs:2, 4, 6 and 20 of Groups 1-3 and 20, respectively, are very similar.

The examiner's attention is respectfully invited to the specification where (1) in the paragraph bridging pages 22 and 23, it is disclosed that SEQ ID NO:4 corresponds to SEQ ID NO:2 in which the 265th and subsequent amino acid residues are removed, and (2) in the paragraph bridging pages 23 and 24, it is disclosed that SEQ ID NO:6 corresponds to SEQ ID NO:2 in which the 249th and

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subsequent amino acid residues are removed. Attached hereto is a table showing that the polypeptides of SEQ ID NOs:2, 4 and 6 all have the same two serine protease consensus sequences as well as an Asp residue between the two consensus sequence. In short, the polypeptides of SEQ ID NO:2, 4, and 6 all have a common serine protease activity, approximately the same size, and extensive sequence identity.

Similarly SEQ ID NO:20 (Group 10), which is a mouse serine protease of approximately the same length as the human polypeptides of SEQ ID NOs:2, 4 and 6, also has both consensus sequences and the Asp residue in between. Furthermore, as can be seen from the attached amino acid alignments, SEQ ID NO:20 has 77.3% sequence homology with SEQ ID NO:2, 4, and 6.

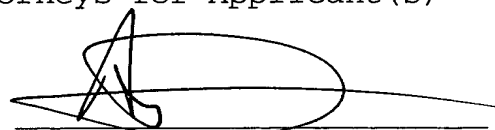
Accordingly, applicants respectfully request that the claims of Groups 1-3 and 10 be examined together on their merits.

Reconsideration and withdrawal of the requirement for restriction insofar as Groups 1-3 and 20 are concerned are respectfully solicited.

Respectfully submitted,

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	Ala-Ala-His-Cys*1	Asp-Ser-Gly-Gly-Pro*2	Asp between *1 and *2
SEQ ID No. 2 (human)	○	○	○
SEQ ID No. 4 (human)	○	○	○
SEQ ID No. 6 (human)	○	○	○
SEQ ID No. 8 (human)	×	×	—
SEQ ID No. 10 (human)	×	○	—
SEQ ID No. 12 (human)	○	×	—
SEQ ID No. 14 (human)	○	×	—
SEQ ID No. 16 (human)	○	×	—
SEQ ID No. 18 (human)	○	×	—
SEQ ID No. 20 (mouse)	○	○	○

[GENETYX-MAC : Amino Acid Sequence Homology Data]

Date : 2003.07.23

1st Amino Acid Sequence

File Name : SEQ. ID. NO.20
Sequence Size : 308

2nd Amino Acid Sequence

File Name : SEQ. ID. NO.2
Sequence Size : 317

Unit Size to compare = 2
Pick up Location = 5

[77.3% / 269 aa]

INT/OPT.Score : < 1209/ 1223 >

1'

MMISRPPPALGGDQFSILILLVLLTSTAPISAATIRVSPDCGKPQQLNRIVGGEDSMD
AQ

* .. * .. ***** .. * .. * .. * .. * .. * .. * .. * .. * .. * ..

1"

MVVS GAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDST
DSE

61'

WPWIVSILKNGSHHCAGSLLTNRWVVTAAHCFKSNMDKPSLFSVLLGAWKLGSPG
PRSQK

***** * .. ***** * .. ***** * .. ***** * .. *****

61"

WPWIVSIQKNGTHHCAGSLLTSRWVITAACFKDNLNKPYLFSVLLGAWQLGNPG
SRSQK

121'

VGIAWVLPHPRYSWKEGTHADIALVRLEHSIQFSERILPICLPDSSVRLPPKTDCWI
AGW

* .. * .. * .. * .. * .. * .. * .. * .. * .. * .. * .. * .. * .. * ..

121"

VGVAWVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWI
SGW

181'
GSIQDGVPLPHPQTLQKLKVPIIDSELCKSLYWRGAGQEAITEGMLCAGYLEGERD
ACLG

*****. * ***** .. *** *****

181"
GSIQDGVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERD
ACLG

241'
DSGGPLMCQVDDHWLLTGIISWGEGCGAQPARCVHQPPSSPLLGAKDRSRGAAAR
VLGGQ

*****. *** *****...

241"
DSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLR
GRAQG

301' WGHKLLI

301" GGALRAPSGSGAAARS

VGVAWVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWI
SGW

181'
GSIQDGVPLPHPQTLQKLKVPIIDSELCKSLYWRGAGQEAITEGMLCAGYLEGERD
ACLG

*****.*****.***.*****

181"
GSIQDGVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERD
ACLG

241'
DSGGPLMCQVDDHWLLTGIISWGEGCGAQPARCVHQPPSSPLLGAKDRSRGAAAR
VLGGQ

*****.***.*****...

241"
DSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKYVQGVQLR
GRAQG

301' WGHKLLI

301" GGALRAPSQSGAPALLCI

VGVAWVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWI
SGW

181'
GSIQDGVPLPHPQTLQKLKVPIIDSELCKSLYWRGAGQEAITEGMLCAGYLEGERD
ACLG

*****.*****.*.*****.***.*****

181"
GSIQDGVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERD
ACLG

241'
DSGGPLMCQVDDHWLLTGIISWGEGCGAQPARCVHQPPSSPLLGAKDRSRGAAAR
VLGGQ

*****.***.*****...

241"
DSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLR
GRPRA

301' WGHKLLI

301" PLLCI